BIOTECH ̲OGY
SYSTEMS
BRANCH

028 C
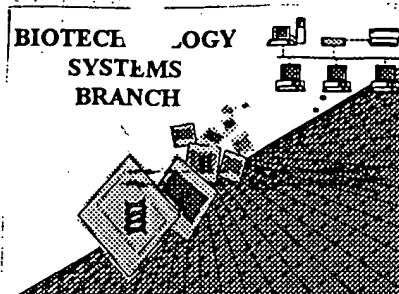
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _O9/676, 2 49_

Source: _O1 PE_

Date Processed by STIC: _10 -10 -00_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

New Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ✓ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)

Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

```
     4 <110> APPLICANT: King, Kendall W
     5         Madura, Rebecca A
     6         Rosey, Everett L
     8 <120> TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF THE MYCOPLASMA PNEUMONIAE
     9         mhp3 GENE AND USES THEREOF
    11 <130> FILE REFERENCE: PC10555
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/676,249
C--> 14 <141> CURRENT FILING DATE: 2000-09-29
    15 <150> PRIOR APPLICATION NUMBER: US 60/156,602
    16 <151> PRIOR FILING DATE: 1999-09-29
    18 <160> NUMBER OF SEQ ID NOS: 41
    20 <170> SOFTWARE: PatentIn Ver. 2.1
```

Does Not Comply
Corrected Diskette Needed
see pp. 1, 2, 3

ERRORED SEQUENCES

```
   153 <210> SEQ ID NO: 3
   154 <211> LENGTH: 1263
   155 <212> TYPE: DNA
   156 <213> ORGANISM: Artificial Sequence
   158 <220> FEATURE:
   159 <223> OTHER INFORMATION: Description of Artificial Sequence: mhp3
   160         manipulated for in vitro expression
   162 <400> SEQUENCE: 3
   163 atgtgggata aagaaacaac taaagaagaa aaatcagccg ataatcaaaa taagcaaatc 60
   164 actgatgtct caaaaatttc aggactagtt aatgaacgaa aatccgaaat tatggccgca 120
   165 aaagctgatg caaacaaaca ttttgggcta aatatggcaa ttgtaaccgc tggtggaacg 180
   166 gtaaatgata attcatttaa ccaatcargt tgggaggcaa ttcaacaact tggcgctctt 240
   167 actggaggtg agattacttc agtagatagt tcaactgctg aacttgaagg aaaatatagc 300
   168 tcacttgcta ataccaacaa aaatgtttgg gtactttctg gttttcaaca cggtgatgcg 360
   169 ttcacaagat ggttaaaaat ccctgaaaat aagcaattat ttactgaaaa aaatattatc 420
   170 atactcggaa ttgactggac tgatactgaa aatgtaattc caacaggtcg atatattaat 480
   171 ttaacctata aaactgaaga agccggatgg cttgcaggat atgcgaatgc ttcctttttg 540
   172 gcaaaaaaat tcccaagtga tccaactaaa agatcagcaa ttgttatcgg tggtgggatt 600
   173 tcgccagctg taactgattt tatcgctggt tatctagccg gaattaaagc ttggaatcta 660
   174 aaaaattctg ataaaaaaac aaagataaca actgataaaa tcgagataaa tcttgggttt 720
   175 gatgttcaag atacttcaac aaaagaaaga cttgaacaaa ttgcttcaaa agataaacct 780
   176 tcaacactat tagctgtcgc tggaccactt actgaaattt tctcggatat aatcgcaaac 840
   177 caaaatgatc gttatctcat tggtgttgac accgaccaat cacttgttta tacaaaaact 900
   178 aaaaataaat ttttcacctc aattttgaaa aatttaggtt actccgtttt cagcgttctt 960
   179 agtgatttat ataccaaaaa atcaaattca agaaatttag ccggctttga atttggtaaa 1020
   180 aaaagtgcaa ccgtttatct tggaattaaa gacaggtttg tcgatattgc tgatacttct 1080
   181 ttagaaggca atgataaaaa actcgcaact gaagccattt ctgaagctaa aaaagaattt 1140
   182 gaagaaaaaa ctaagacaat tcctgccgaa gaagttcgta aaactttaga aattccggaa 1200
   183 atgcctgata aacaacctga taagcaacag gaaagcttag acaaactaat taccgatatt 1260
E--> 184 aataatcta                                                 1263
```

Number of bases conflict:
1263 listed
1269 shown

```
<210> 7
<211> 14
<212> PRT
<213> Mycoplasma hyopneumoniae

<400> 7
Ala Gly (Xaa) Trp Ala Lys Glu Thr Thr Lys Glu Glu Lys Ser
 1            5                10              .
```

Missing mandatory <220> to <223> features to explain "Xaa" in sequence. See #10 on Error Summary Sheet.

```
<210> 10
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide

<400> 10
tgytgrgcna argaracnac naargargar                                    30
```

Missing mandatory <220> to <223> features to explain "n's" in sequence. See #10 on Error Summary Sheet.

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 10/10/2000
PATENT APPLICATION: US/09/676,249   TIME: 16:31:43

Input Set : A:\PC10555A-SEQ-LIST.txt
Output Set: N:\CRF3\10102000\I676249.raw

```
L:13  M:270 C: Current Application Number differs, Replaced Application Number
L:14  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:184 M:254 E: No. of Bases conflict, LENGTH:Input:1263 Counted:1269 SEQ:3
L:184 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1263 Found:1269 SEQ:3
L:275 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:275 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:275 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:350 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:350 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:350 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:350 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:350 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
L:395 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:395 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:395 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
L:421 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:12
L:421 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:12
L:421 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12
L:447 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
L:447 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:447 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
```